

1600

## RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/09/597,796B

TIME: 12:32:10

Input Set : A:\-90-5.app

Output Set: N:\CRF3\01152002\I597796B.raw

Does Not Comply  
Corrected Diskette Needed

PP. 3, 6-8

3 <110> APPLICANT: Skeiky, Yasir  
 4 Reed, Steven  
 5 Alderson, Mark  
 6 Corixa Corporation  
 8 <120> TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis  
 10 <130> FILE REFERENCE: 014058-009050US  
 12 <140> CURRENT APPLICATION NUMBER: US 09/597,796B  
 13 <141> CURRENT FILING DATE: 2001-06-20  
 15 <150> PRIOR APPLICATION NUMBER: US 09/056,556  
 16 <151> PRIOR FILING DATE: 1998-04-07  
 18 <150> PRIOR APPLICATION NUMBER: US 09/223,040  
 19 <151> PRIOR FILING DATE: 1998-12-30  
 21 <150> PRIOR APPLICATION NUMBER: WO PCT/US99/07717  
 22 <151> PRIOR FILING DATE: 1999-04-07  
 24 <150> PRIOR APPLICATION NUMBER: US 09/287,849  
 25 <151> PRIOR FILING DATE: 1999-04-07  
 27 <150> PRIOR APPLICATION NUMBER: US 60/158,338  
 28 <151> PRIOR FILING DATE: 1999-10-07  
 30 <150> PRIOR APPLICATION NUMBER: US 60/158,425  
 31 <151> PRIOR FILING DATE: 1999-10-07  
 33 <160> NUMBER OF SEQ ID NOS: 30  
 35 <170> SOFTWARE: PatentIn Ver. 2.1  
 37 <210> SEQ ID NO: 1  
 38 <211> LENGTH: 588  
 39 <212> TYPE: DNA  
 40 <213> ORGANISM: Mycobacterium tuberculosis  
 42 <220> FEATURE:  
 43 <223> OTHER INFORMATION: Ra35, N-terminus of MTB32A (TbRa35FL)  
 45 <220> FEATURE:  
 46 <221> NAME/KEY: CDS  
 47 <222> LOCATION: (1)..(588)  
 48 <223> OTHER INFORMATION: Ra35  
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 52 tccgcgatgg tcgccccagt ggggccacag gtggtcaaca tcaacaccaa actgggctac 120  
 53 aacaacgccg tgggcgcggg gaccggcatc gtcatcgatc ccaacggtgt cgtgctgacc 180  
 54 aacaaccacg tgatcgcggg cgccaccgac atcaatgcgt tcagcgctcg ctccggccaa 240  
 55 acctacggcg tcgatgtggt cgggtatgac cgcaaccagg atgtcgcggt gctgcagctg 300  
 56 cgcggtgccg gtggcctacc atcggcgggc atcgggtggc gcgtcgcggt tggtagagccc 360  
 57 gtcgtcgcca tgggcaacag cgggtggcag ggcggaacgc cccgtgcggt gcctggcagg 420  
 58 gtggtcgcgc tcggccaaac cgtgcaggcg tcggattcgc tgaccggtgc cgaagagaca 480  
 59 ttgaacgggt tgatccagtt cgatgccgcg atccagcccg gtgattcggg cgggcccgctc 540  
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 63 <210> SEQ ID NO: 2  
 64 <211> LENGTH: 195  
 65 <212> TYPE: PRT  
 66 <213> ORGANISM: Mycobacterium tuberculosis

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Input Set : A:\-90-5.app

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67 &lt;223&gt; OTHER INFORMATION: Ra35, N-terminus of MTB32A (TbRa35FL)

70 &lt;400&gt; SEQUENCE: 2

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74           20           25           30
75 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
76           35           40           45
77 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
78           50           55           60
79 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
80   65           70           75           80
81 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
82           85           90           95
83 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
84           100          105          110
85 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
86           115          120          125
87 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
88           130          135          140
89 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
90   145          150          155          160
91 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
92           165          170          175
93 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
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95 Ala Ala Ser
96           195

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99 &lt;210&gt; SEQ ID NO: 3

100 &lt;211&gt; LENGTH: 1872

101 &lt;212&gt; TYPE: DNA

102 &lt;213&gt; ORGANISM: Mycobacterium tuberculosis

104 &lt;220&gt; FEATURE:

105 &lt;223&gt; OTHER INFORMATION: MTB32A (TbRa35FL) cDNA

107 &lt;400&gt; SEQUENCE: 3

P.3

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110 gtcattggtg ctgagcgtgc tggctgccgt cgggctgggc ctggccacgg cgccggccca 180
111 ggcgggcccc cgggccttgt cgcaggaccg gttcgccgac ttccccgcgc tgcccctcga 240
112 cccgtccgcg atggtcgccc aagtggcgcc acagggtggtc aacatcaaca ccaaactggg 300
113 ctacaacaac gccgtgggcg ccgggaccgg catcgtcacg gatcccaacg gtgtcgtgct 360
114 gaccaacaac cacgtgatcg cgggcgccac cgacatcaat gcgttcagcg tcggctccgg 420
115 ccaaacctac ggcgtcgatg tggtcgggta tgaccgcacc caggatgtcg cgggtgctga 480
116 gctgcgcggt gccgtgggcc tgccgtcggc ggcgatcggt ggcggcgctc cggttggtga 540
117 gcccgtcgtc gcgatgggca acagcgggtg gcaggggcga acgccccgtg cgggtgcctg 600
118 cagggtggtc gcgctcggcc aaaccgtgca ggcgtcggat tcgctgaccg gtgccgaaga 660
119 gacattgaac gggttgatcc agttcgatgc cgcaatccag cccggtgatt cggggcgggc 720
120 cgtcgtcaac ggcctaggac aggtggtcgg tatgaacacg gccgcgtccg ataacttcca 780
121 gctgtccacg ggtgggcagg gattcgccat tccgatcggg caggcgatgg cgatcgcggg 840

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Input Set : A:\-90-5.app

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123 cttgggtggt gtcgacaaca acggcaacgg cgcacgagtc caacgcgtgg tcggaagcgc 960
124 tccggcggca agtctcggca tctccaccgg cgacgtgac accgcggtcg acggcgctcc 1020
125 gatcaactcg gccaccgcga tggcggagcg gcttaacggg catcatcccg gtgacgtcat 1080
126 ctcggtgaac tggcaaacca agtcggggcg cagcgtgaca gggaaacgtga cattggccga 1140
127 gggacccccg gcctgatttg tcgcggtac caccgcggcg ccggccaatt ggattggcgc 1200
128 cagccgtgat tgccgcgtga gcccccgagt tccgtctccc gtgcgcgtgg cattgtggaa 1260
129 gcaatgaacg aggcagaaca cagcgttgag caccctcccg tgcagggcag ttacgtcgaa 1320
130 ggcggtgtgg tcgagcatcc ggaatgccaag gacttcggca gcgcgcgcgc cctgccgcgc 1380
131 gatccgacct ggtttaagca cgcgctcttc tacgaggtgc tggctccggc gttcttcgac 1440
W--> 132 gccagcgcgg acggttccg cgactcgcgt ggactcatcg atcgctcga ctacctgcag 1500
133 tggcttgcca tcgactgcat ctggtgcgcgc cgttcctacg actcaccgct gcgcgacggc 1560
134 ggttacgaca ttgcgcactt ctacaagggt ctgccogaat tcggcaccgt cgacgatttc 1620
135 gtcgccctgg tcgacaccgc tcaccggcga ggtatccgca tcacacccga cctggtgatg 1680
136 aatcacacct cggagtcgca cccctggttt caggagtcgc gccgcgaccc agacggaccg 1740
137 tacggtgact attacgtgtg gacgcacacc agcgcgcgt acaccgacgc ccggtatcgc 1800
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139 gcaccgattc tt 1872
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143 <211> LENGTH: 355
144 <212> TYPE: PRT
145 <213> ORGANISM: Mycobacterium tuberculosis
147 <220> FEATURE:
148 <223> OTHER INFORMATION: MTB32A (TbRa35FL) protein
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154 20 25 30
155 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
156 35 40 45
157 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
158 50 55 60
159 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
160 65 70 75 80
161 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
162 85 90 95
163 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
164 100 105 110
165 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
166 115 120 125
167 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
168 130 135 140
169 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
170 145 150 155 160
171 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
172 165 170 175
173 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Thr
174 180 185 190

```

→ see  
item 9  
on  
Error  
summary  
sheet

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DATE: 01/15/2002

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TIME: 12:32:10

Input Set : A:\-90-5.app

Output Set: N:\CRF3\01152002\I597796B.raw

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175 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
176          195          200          205
177 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
178      210          215          220
179 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
180 225          230          235          240
181 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
182          245          250          255
183 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
184          260          265          270
185 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
186      275          280          285
187 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
188      290          295          300
189 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
190 305          310          315          320
191 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
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195 Pro Pro Ala
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202 <213> ORGANISM: Mycobacterium tuberculosis
204 <220> FEATURE:
205 <223> OTHER INFORMATION: MTBRa12 C-terminus of MTB32A (Ra35FL)
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210 caccgttcat atcgggccta ccgccttccct cggcttgggt gttgtcgaca acaacggcaa 180
211 cggcgacaga gtccaacgcg tggtcgggag cgctccggcg gcaagtctcg gcatctccac 240
212 cggcgacgtg atcaccgcgg tcgacggcgc tccgatcaac tcggccaccg cgatggcgga 300
213 cgcgcttaac gggcatcatc ccggtgacgt catctcgggt aactggcaaa ccaagtcggg 360
214 cggcacgcgt acaggggaac tgacattggc cgagggaccc ccggcctgat ttcgtcgygg 420
215 ataccacccg ccggccggcc aattgga 447
218 <210> SEQ ID NO: 6
219 <211> LENGTH: 132
220 <212> TYPE: PRT
221 <213> ORGANISM: Mycobacterium tuberculosis
223 <220> FEATURE:
224 <223> OTHER INFORMATION: MTBRa12 C-terminus of MTB32A (Ra35FL)
226 <400> SEQUENCE: 6
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229 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
230      20          25          30
231 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly

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## RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/09/597,796B

TIME: 12:32:10

Input Set : A:\-90-5.app

Output Set: N:\CRF3\01152002\I597796B.raw

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232          35          40          45
233 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
234          50          55          60
235 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
236 65          70          75          80
237 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
238          85          90          95
239 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
240          100          105          110
241 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
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243 Gly Pro Pro Ala
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248 <211> LENGTH: 3058
249 <212> TYPE: DNA
250 <213> ORGANISM: Mycobacterium tuberculosis
252 <220> FEATURE:
253 <223> OTHER INFORMATION: MTB39 (TbH9) cDNA full-length
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258 tgtggctagc aatgccgctg cgggcgcccc gacgactggg gtggtgcccc ccgctgccga 180
259 tgaggtgtcg gcgctgactg cgggcgacct cgccgcacat gcggcgatgt atcagtccgt 240
260 gagcgctcgg gctgctgcga ttcattacca gttcgtggcc acccttgcca gcagcgccag 300
261 ctcgatgctg gccactgaag tcgccaatgc gggcgggccc agctaagcca ggaacagtcg 360
262 gcacgagaaa ccacgagaaa tagggacacg taatggtgga tttcggggcg ttaccaccgg 420
263 agatcaactc cgcgaggatg tacgcccggc cgggttcggc ctcgctggtg gccgcggtc 480
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265 tctggggtct gacggtgggg tcgtggatag gttcgtcgcc gggctctgat gtggcgggcg 600
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267 aggtccgggt tgcgtcgggc gcctacgaga cggcgatagg gctgacgggt cccccggcg 720
268 tgatcgccga gaaccgtgct gaactgatga ttctgatagc gaccaacctc ttggggcaaa 780
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270 ccgcgatggt tggctacgcc gcggcgacgg cgacggcgac ggcgacgttg ctgccgttcg 900
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274 cggctctgcc gcacggtcg ccgatcagca acatggtgtc gatggccaac aaccacatgt 1140
275 cgatgaccaa ctcggtgtg tcgatgacca acaccttag ctcgatgttg aagggctttg 1200
276 ctccggcggc ggccgcccag gccgtgcaaa ccgcgggcga aaacggggtc cggcgatga 1260
277 gctcgctggg cagctcgctg ggttcttcgg gtctggggcg tgggggtggc gccaaacttg 1320
278 gtcggcgggc ctcggtcggt tcgttgcgg tgccgcaggc ctggggccgc gccaaaccag 1380
279 cagtcacccc ggcggcgcg gcgctgccgc tgaccagcct gaccagcgcc gcgaaagag 1440
280 ggcccgggca gatgctgggc gggctgccgg tggggcagat gggcgccagg gccggtggtg 1500
281 ggctcagtg tggtctgct gtcccgccgc gacctatgt gatgccgat tctccggcg 1560
282 ccggctagga gagggggcg agactgtcgt tatttgacca gtgatcgcg gtctcggtgt 1620
283 ttccgcggcc ggctatgaca acagtcaatg tgcattgaca gttacaggta ttaggtccag 1680
284 gttcaacaag gagacaggca acatggcctc acgttttatg acgatccgc acgcgatgcg 1740

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097597,796B 6

<210> 10

<211> 596

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: fusion  
protein TbH9-Ra35 (MTB59F)

<400> 10

> <2207 < insert this  
mandatory  
numeric identifier  
whenever <2217, <2227,  
or <2237 is  
shown  
↓

The types of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

<210> 11  
 <211> 2287  
 <212> DNA  
 <213> Mycobacterium tuberculosis  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: fusion  
 protein Ra12-TbH9-Ra35 (MTB72F)

<213> can only have one response:

Artificial Sequence  
or Unknown or  
 Scientific name  
 (Genus/species)

<210> 25  
 <211> 851  
 <212> DNA  
 <213> Mycobacterium tuberculosis

<220>  
 <223> MTB39 (TbH9) cDNA

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 cgccgagAAC cgtgctgaac tgatgattct gatagcgacc aacctcttgg ggcaaaacac 180  
 cccggcgatc gcggtcaacg aggccgaata cggcgagatg tgggcccAag acgccgccgc 240  
 gatgtttggc tacgccgcgg cgacggcgac ggcgacggcg acgttgctgc cgttcgagga 300  
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 ctgccgcat cggtcgccga tcagcaacat ggtgtcgatg gccaacaacc acatgtcgat 540  
 gaccaactcg ggtgtgtcga tgaccaaacac cttgagctcg atgttgAagg gctttgctcc 600  
 ggcggcgccc gcccaggccg tgcaaaccgc ggcgcaaaac ggggtccggg cgatgagctc 660  
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 ggcggcctcg gtacggtatg gtcaccggga tggcggaAAA tatgcaagt ~~ctggtcggcg~~ 780  
 gaacggtggt ccggcgtaag gtttaccccc gttttctgga tgcggtgaac ttcgtcaacg 840  
 gaaacagtta c 851

→ see  
 item 9  
 on Error  
 Summary  
 sheet

IMPORTANT  
 →

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/597,796B

DATE: 01/15/2002

TIME: 12:32:11

Input Set : A:\-90-5.app

Output Set: N:\CRF3\01152002\I597796B.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:132 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3  
 L:132 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3  
 L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
 L:138 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3  
 L:138 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3  
 L:138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
 L:421 M:258 W: Mandatory Feature missing, <220> FEATURE: ✓  
 L:508 M:280 W: Numeric Identifier already exists, Organism not replaced. ✓  
 L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
 L:572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 ✓  
 L:580 M:258 W: Mandatory Feature missing, <220> FEATURE: ✓  
 L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
 L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 ✓  
 L:804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
 L:805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
 L:1082 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25  
 L:1082 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25  
 L:1082 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
 L:1126 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26  
 L:1126 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
 L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
 L:1181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27